

**Amendments to Specification**

Please replace the following paragraphs:

**Paragraph beginning on page 39, line 15**

Amplification was carried out in two steps. The first amplification reaction was performed using 1 µL of first strand cDNA and primer set one (SEQ ID NO:11 and SEQ ID NO:12) with 30 cycles of 94°C for 30 seconds, 50°C for 30 seconds and 72°C for one minute. A second amplification reaction was done with 1 µL of the resulting product with primer set two (SEQ ID NO:13 and SEQ ID NO:14) and using 30 cycles of 94°C for 30 seconds, 50.5°C for 30 seconds and 72°C for one minute. The resulting PCR sequence was cloned into pCR2.1 using TOPO™ TA Cloning Kit (Invitrogen). Plasmid DNA was purified using QIAFilter cartridges (Qiagen Inc) or Wizard Plus Minipreps DNA Purification System (Promega) following the manufacturer's instructions. Sequence was generated on an ABI Automatic sequencer using dye terminator technology and using a combination of vector and insert-specific primers. Sequence editing was performed using DNASTAR (DNASTAR, Inc.). All sequences represent coverage at least two times in both directions. The nucleotide sequence comprising the cDNA insert in clone sugarbeet 1 is shown in SEQ ID NO:47; the deduced amino acid sequence of this DNA is shown in SEQ ID NO:48. The nucleotide sequence comprising the cDNA insert in clone sugarbeet 2 is shown in SEQ ID NO:60[[61]]; the deduced amino acid sequence of this DNA is shown in SEQ ID NO:61.

**Paragraph beginning on page 41, line 13:**

A consensus sequence was determined by aligning the amino acid sequences of the present invention using the Clustal method of alignment and this sequence is shown in SEQ ID NO:66. Amino acids not conserved are indicated by Xaa. These are:

Xaa <sub>10</sub>	Phe or Leu
Xaa <sub>16</sub>	Ser or Leu
Xaa <sub>23</sub>	Ser or Thr
Xaa <sub>25</sub>	Ile or Lys
Xaa <sub>39</sub>	Lys or Arg
Xaa <sub>48</sub>	Pro or Leu
Xaa <sub>60</sub>	Pro or Leu
Xaa <sub>73</sub>	Leu or His
Xaa <sub>74</sub>	Ser or Tyr
Xaa <sub>95</sub>	Ala or Thr

Xaa <sub>96</sub>	Asn or His
Xaa <sub>102</sub>	Asn or Ser
Xaa <sub>110</sub>	Ile, Val, or Thr
Xaa <sub>112</sub>	Arg or His
Xaa <sub>117</sub>	Asn or Ser
Xaa <sub>118</sub>	Ser or Leu
Xaa <sub>121</sub>	Met or Arg
Xaa <sub>122</sub>	Ala or Val
Xaa <sub>124</sub>	Phe or Ile
Xaa <sub>129</sub>	Lys or Arg
Xaa <sub>147</sub>	Lys or Glu
Xaa <sub>159</sub>	Leu or Phe
Xaa <sub>162</sub>	Ala or Val
Xaa <sub>166</sub>	Ser or Gly
Xaa <sub>170</sub>	Gln or Arg
Xaa <sub>175</sub>	Val or Leu
Xaa <sub>183</sub>	Ala or Thr
Xaa <sub>187</sub>	Thr or Ile
Xaa <sub>191</sub>	Met or Val
Xaa <sub>209</sub>	Phe or Tyr
Xaa <sub>219</sub>	Arg or Trp
Xaa <sub>223</sub>	Tyr or His
Xaa <sub>253</sub>	Gly or Glu
Xaa <sub>259</sub>	Lys or Glu
Xaa <sub>263</sub>	Val or Asp
Xaa <sub>264</sub>	Val, Asp, or Ile
Xaa <sub>268</sub>	Ala or Val
Xaa <sub>272</sub>	Phe or Leu
Xaa <sub>285</sub>	Thr or Met
Xaa <sub>293</sub>	<u>Glu or Asp</u>
Xaa <sub>292</sub>	<u>Glu or Asp</u>
Xaa <sub>293</sub>	<u>Gln or His</u>
Xaa <sub>294</sub>	<u>Thr or Ile</u>
Xaa <sub>294</sub>	<del>Thr, or Ile</del>
Xaa <sub>301</sub>	Phe or Leu
Xaa <sub>306</sub>	Thr or Ile
Xaa <sub>311</sub>	Val or Glu
Xaa <sub>312</sub>	Val or Ala

Xaa<sub>325</sub> Arg or Lys  
Xaa<sub>328</sub> Gln or Glu  
Xaa<sub>329</sub> Lys or Arg  
Xaa<sub>334</sub> Val or Ala  
Xaa<sub>342</sub> Arg or Ile  
Xaa<sub>377</sub> Thr or Ile  
Xaa<sub>381</sub> Glu or Gly  
Xaa<sub>385</sub> Tyr, His, or Cys  
Xaa<sub>387</sub> Ile or Thr  
Xaa<sub>393</sub> Val or Ile  
Xaa<sub>394</sub> Leu or Pro  
Xaa<sub>402</sub> Arg or Lys  
Xaa<sub>404</sub> Ser or Pro  
Xaa<sub>413</sub> Ser or Phe  
Xaa<sub>422</sub> Glu or Gly  
Xaa<sub>428</sub> Gly or Arg  
Xaa<sub>429</sub> Pro or Leu  
Xaa<sub>435</sub> Gln or Arg  
Xaa<sub>447</sub> Arg or Gly  
Xaa<sub>453</sub> Asn, Ser, or Ile  
Xaa<sub>459</sub> Met or Thr, and  
Xaa<sub>485</sub> Asp or Gly

**Please replace the sequence listing with the enclosed amended sequence listing.**